CLAIMS

1. An analysis system for capturing target molecules in a sample, the system comprising:

(a) supports with a largest dimension of 500 μm or less, wherein each support includes at least one capture analyte bound thereto, said at least one analyte being at least one capture agent exhibiting an affinity for one or more of proteins, antibodies, antibody fragments, DNA aptamers, nucleic acids, small molecules and any other molecules used to bind target molecules;

(b) engaging means for introducing said sample into contact with said at least one analyte of at least one support in a fluid solution, such that binding of at least one target molecule with at least one analyte is indicative of the presence of said at least one target molecule;

characterised in that:

(c) each support comprises identifying means for enabling the system to identify the support;

(d) the system includes interrogating means for detecting binding of said at least one target molecule with said at least one analyte, the system thereby being capable of associating each support with its corresponding target molecule; and

(e) the system further including analysis means for recovering and analysing a remainder of said sample whose molecules are not susceptible to capture by said at least one analyte bound to said supports.

2. A system according to Claim 1, wherein at least one target molecule captured onto its corresponding at least one analyte is reversibly bound thereto such that said at least one reversibly bound molecule is susceptible to being recovered, characterised and quantitated using said interrogating means.

3. A system according to Claim 1 or 2, wherein the amount of target molecule present in the sample is quantitable from the amount thereof bound to said at least one capture analyte.

4. A system according to Claim 1, 2 or 3, wherein the analysis means for analysing the remainder of the sample includes one or more of the following for performing such analysis: microarrays, mass spectrophoto,etry, 2D-GE, chromatography, sequencing, flow cytometry and immunoprecipitation.

5. A system according to Claim 1, 2, 3 or 4, wherein the largest dimension of the support is less than 300 μm.

6. A system according to any one of the preceding claims, wherein the largest dimension of the support is less than 150μm.

7. A system according to any one of the preceding claims, wherein the largest dimension of the support is less than 50 μm.

8. A system according to any one of the preceding claims, wherein the identifying means comprises one or more of distinguishing geometrical features, such as shape, size, barcode or dotcode, enabling identification of each support.

9. A system according to any one of the preceding claims, wherein at least one of the identification means is a radio frequency identification transponder (RFID).

10. A system according to any one of the preceding claims, wherein at least one of the identification means is an optical identification, such as fluorescence or colour based.

11. A system according to any one of the preceding claims, wherein the fluid solution is a liquid.

12. A method of capturing and filtering target molecules in a sample, the method including the steps of:

(a) providing supports with a largest dimension of 500 μm or less, wherein each support includes at least one capture analyte bound thereto, said at least one analyte being at least one capture agent exhibiting an affinity for one or more of proteins, antibodies, antibody fragments, DNA aptamers, nucleic acids, small molecules and any other molecules used to bind target molecules;

(b) introducing said sample into contact with said at least one analyte of at least one support in a fluid solution, such that binding of at least one target molecule with at least one analyte is indicative of the presence of said at least one target molecule;

characterised in that the method further comprises the step of:

(c) providing each support with identifying means for enabling identification of the support;

(d) detecting binding of said at least one target molecule with said at least one analyte, thereby associating each support with its corresponding target molecule; and

(e) recovering and analysing a remainder of said sample whose molecules are not susceptible to capture by said at least one analyte bound to said supports.

13. A method according to Claim 12, wherein at least one target molecule captured onto its corresponding at least one analyte is reversibly bound thereto such that said at least one reversibly bound molecule is susceptible to being recovered, characterised and quantitated using interrogating means.

14. A method according to Claim 12 or 13, wherein the amount of target molecule present in the sample is quantitable from the amount thereof bound to said at least one capture analyte.

15. A method according to Claim 12, 13, or 14, wherein in step (e) the remainder of the sample is analysed using one or more of the following: microarrays, mass spectrophoto,etry, 2D-GE, chromatography, sequencing, flow cytometry and immunoprecipitation.

16. A method according to Claim 12, 13, 14, or 15, wherein the largest dimension of the support is less than 300 μm.

17. A method according to any one of Claims 12 to 16, wherein the largest dimension of the support is less than 150μm.

18. A method according to any one of Claims 12 to 17, wherein the largest dimension of the support is less than 50 μm.

19. A method according to any one of Claims 12 to 18, wherein the identifying means comprises one or more of distinguishing geometrical features, such as shape, size, barcode or dotcode, enabling identification of each support.

20. A method according to any one of Claims 12 to 19, wherein at least one of the identifying means is a radio frequency identification transponder (RFID).

21. A method according to any one of Claims 12 to 20, wherein at least one of the identifying means is an optical identification, such as fluorescence or colour based.

22. A method according to any one of Claims 12 to 21, wherein the fluid solution is a liquid.

23. A system for reversibly capturing target molecules for the purpose of reducing sample complexity and to characterise the captured molecules hereinbefore described with reference to one or more of Figures 1 to 8.

24. A method of reversibly capturing target molecules for the purpose of reducing sample complexity and to characterise the captured molecules hereinbefore described with reference to one or more of Figures 1 to 8.